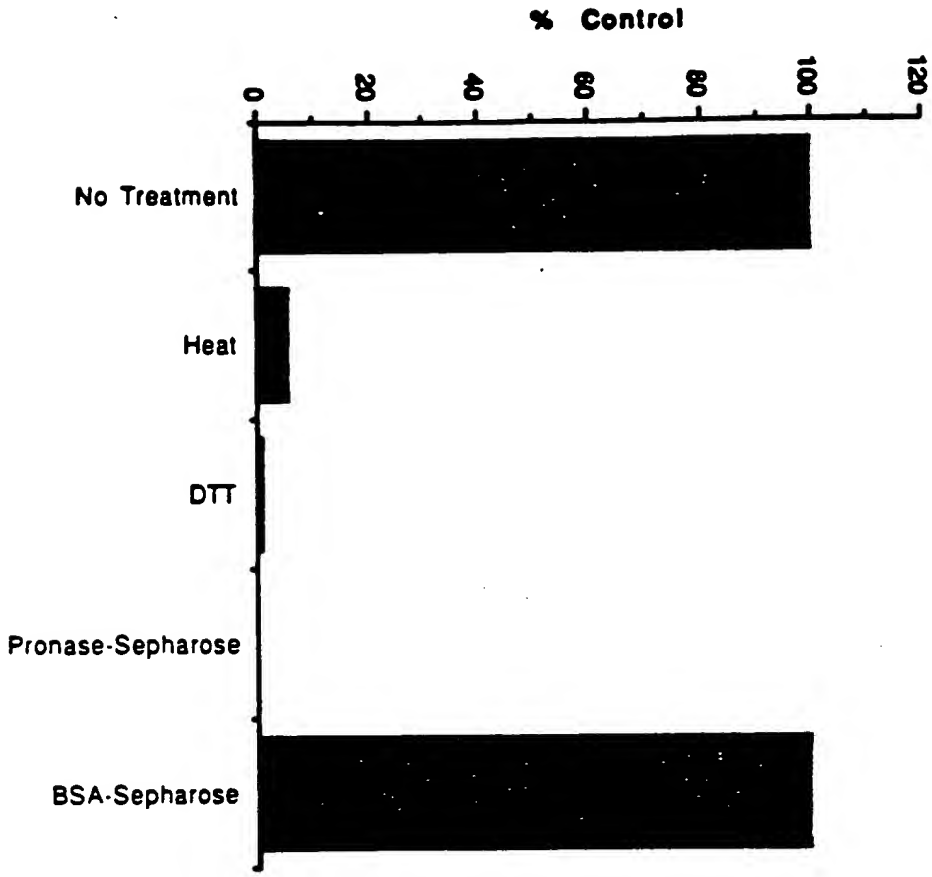

% Control
0
20
40
60
80
100
120
No Treatment
Heat
DTT
Pronase-Sepharose
BSA-Sepharose

Figure 1

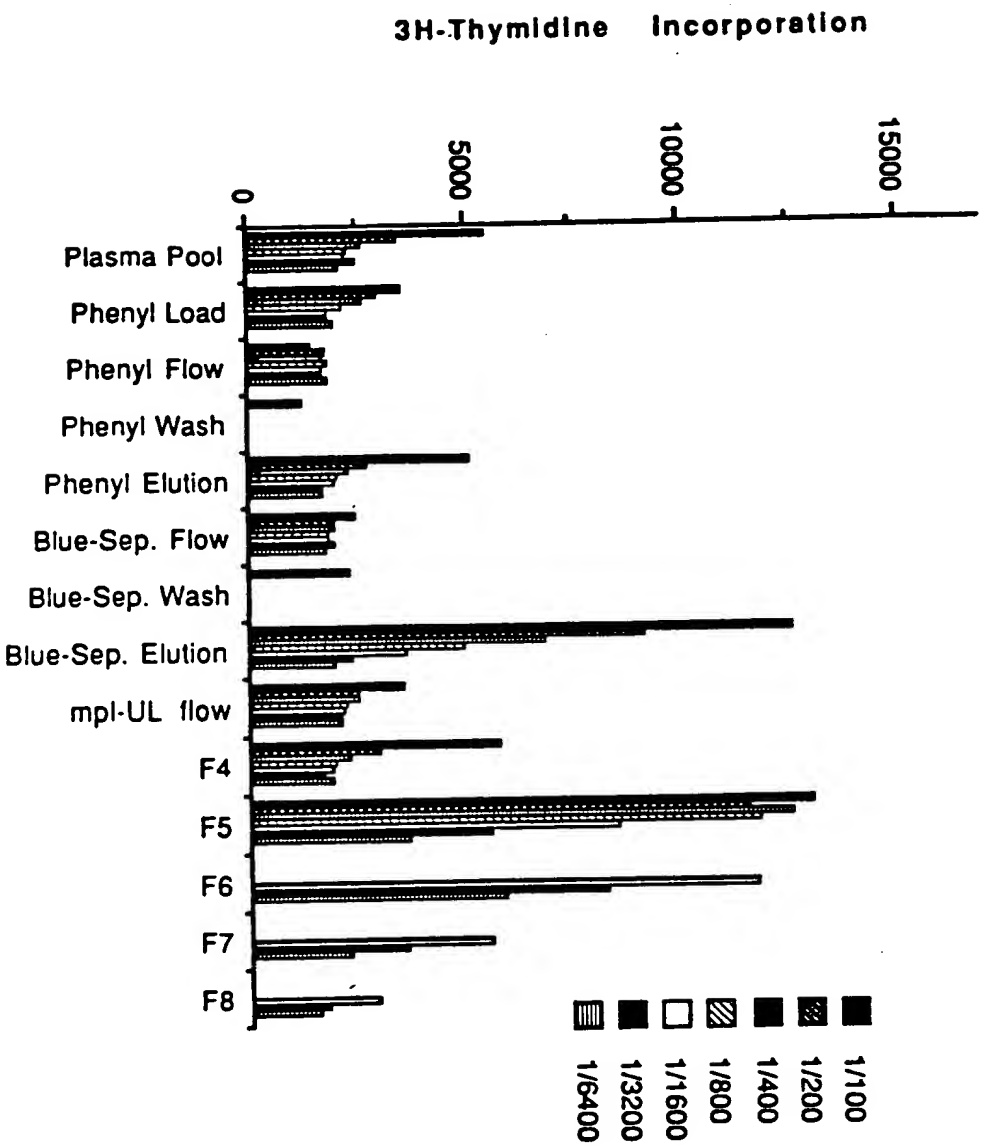

3H-Thymidine Incorporation
0
5000
10000
15000
Plasma Pool
Phenyl Load
Phenyl Flow
Phenyl Wash
Phenyl Elution
Blue-Sep. Flow
Blue-Sep. Wash
Blue-Sep. Elution
mpl-UL flow
F4
F5
F6
F7
F8
1/6400
1/3200
1/1600
1/800
1/400
1/200
1/100

Figure 2

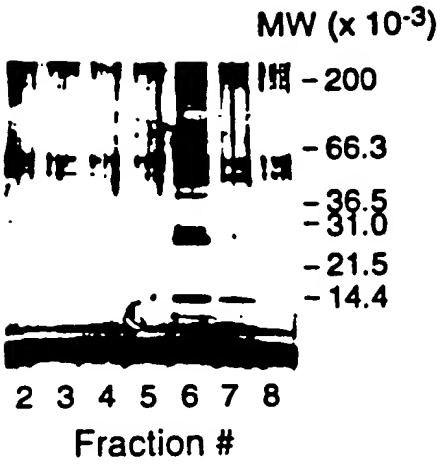


Figure 3

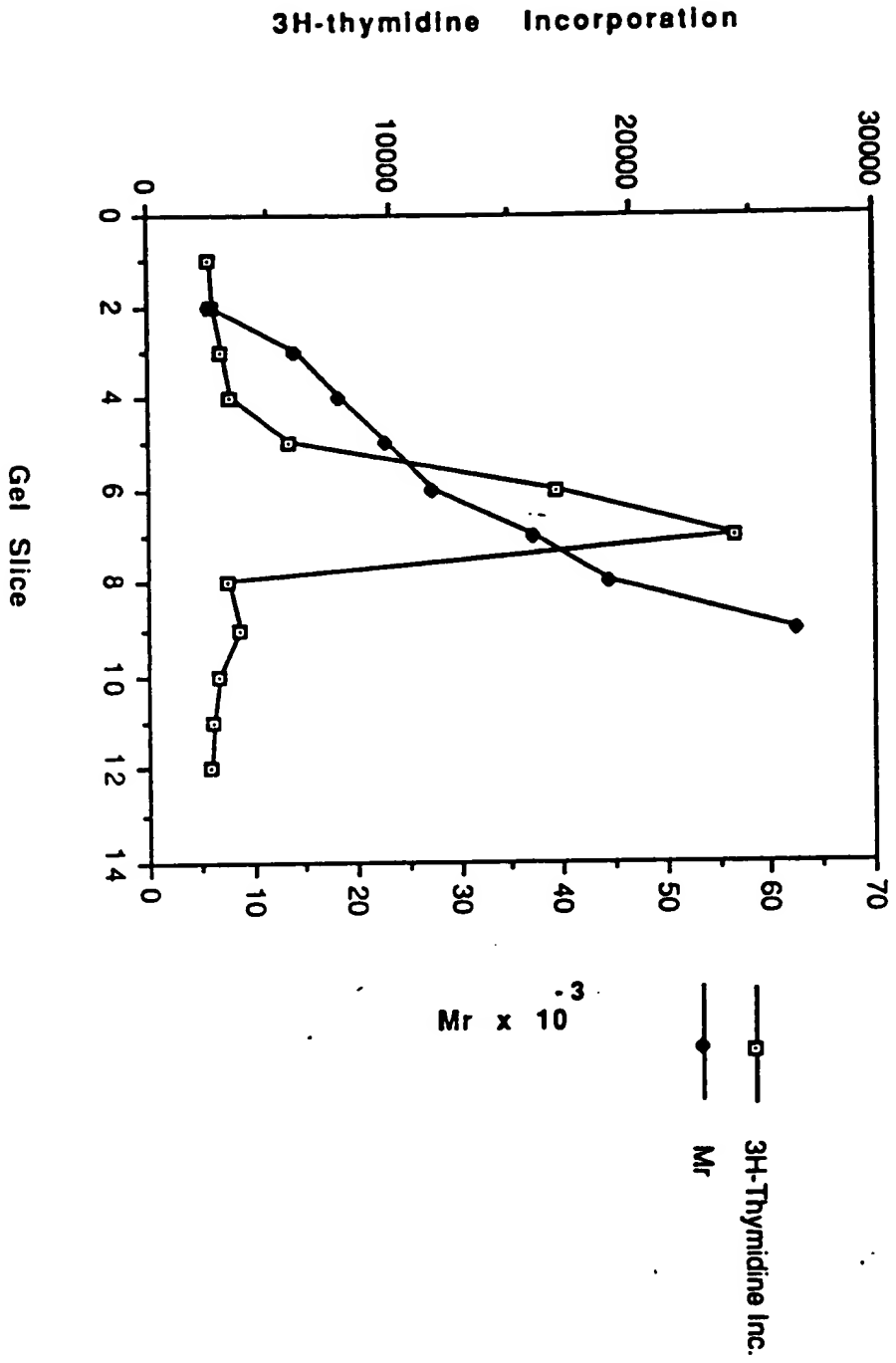

3H-thymidine Incorporation
Gel Slice
Mr x 10 -3
Mr
3H-Thymidine Inc.

Figure 4

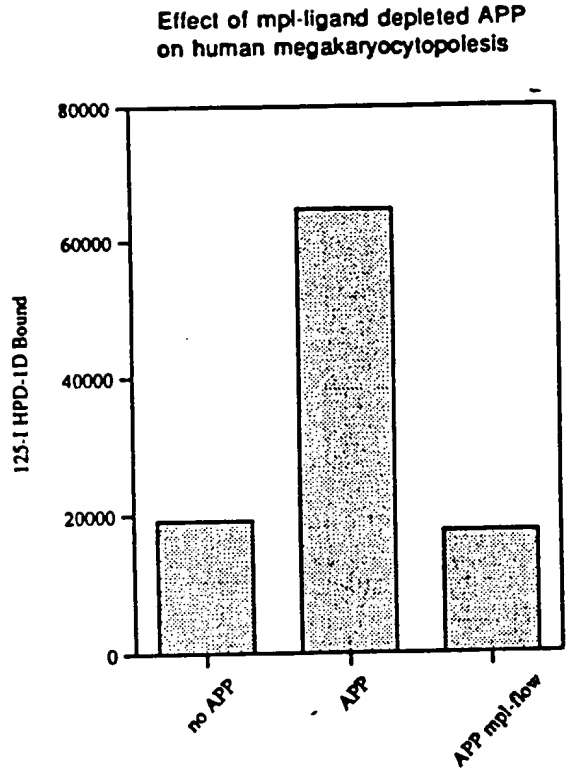

Effect of mpl-ligand depleted APP
on human megakaryocytopolesis
125-I HPD-1D Bound
80000
60000
40000
20000
0
no APP
APP
APP mpl-flow

Figure 5

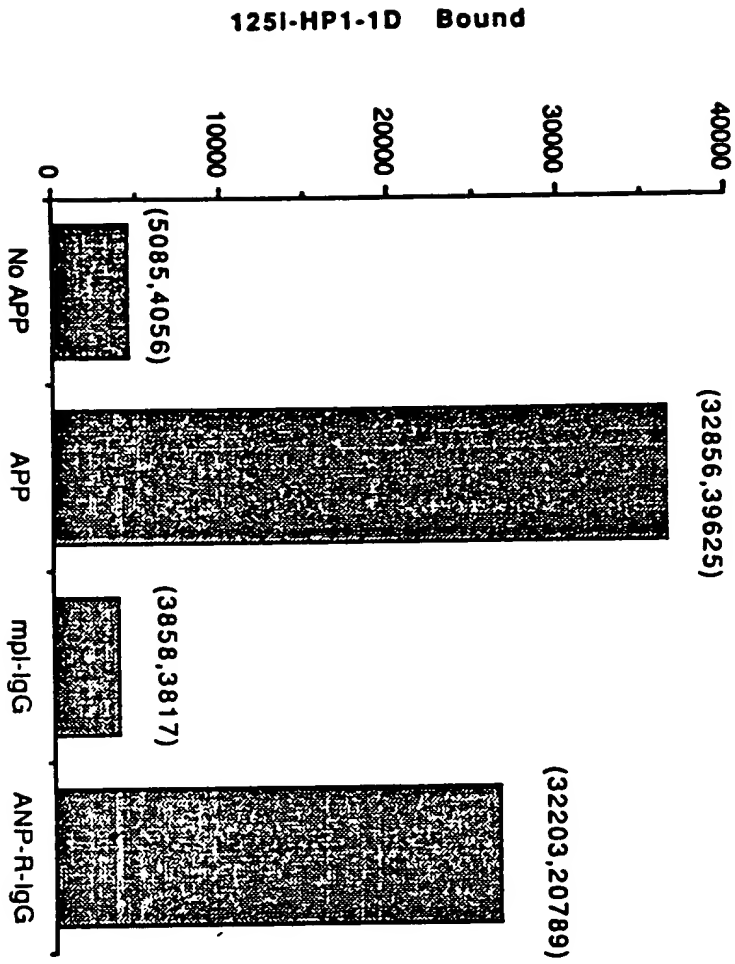

125I-HP1-1D Bound
0
10000
20000
30000
40000
No APP
(5085,4056)
APP
(32856,39625)
mpl-IgG
(3858,3817)
ANP-R-IgG
(32203,20789)

Figure 6

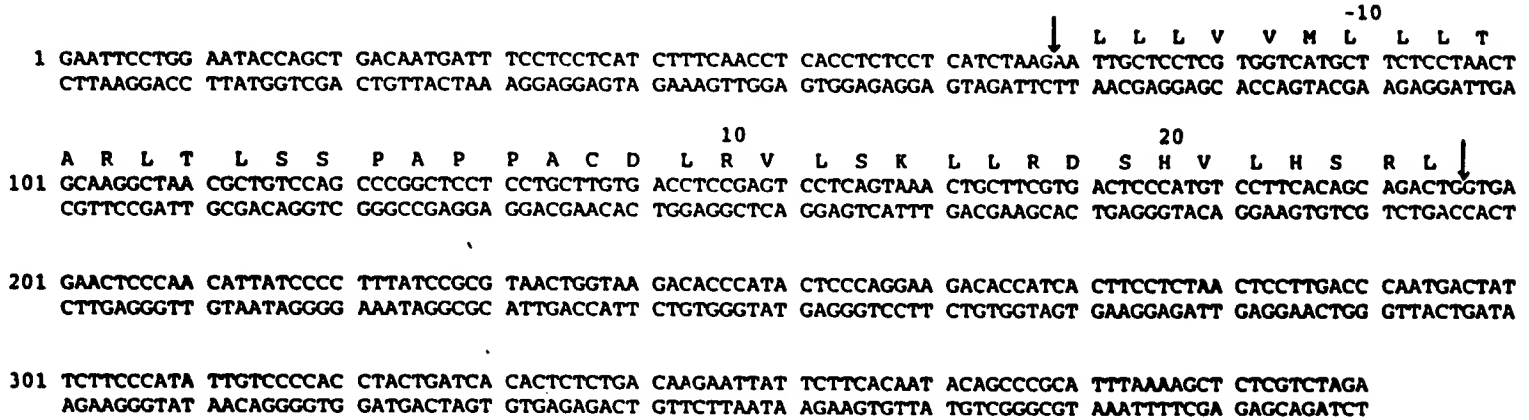


Figure 7

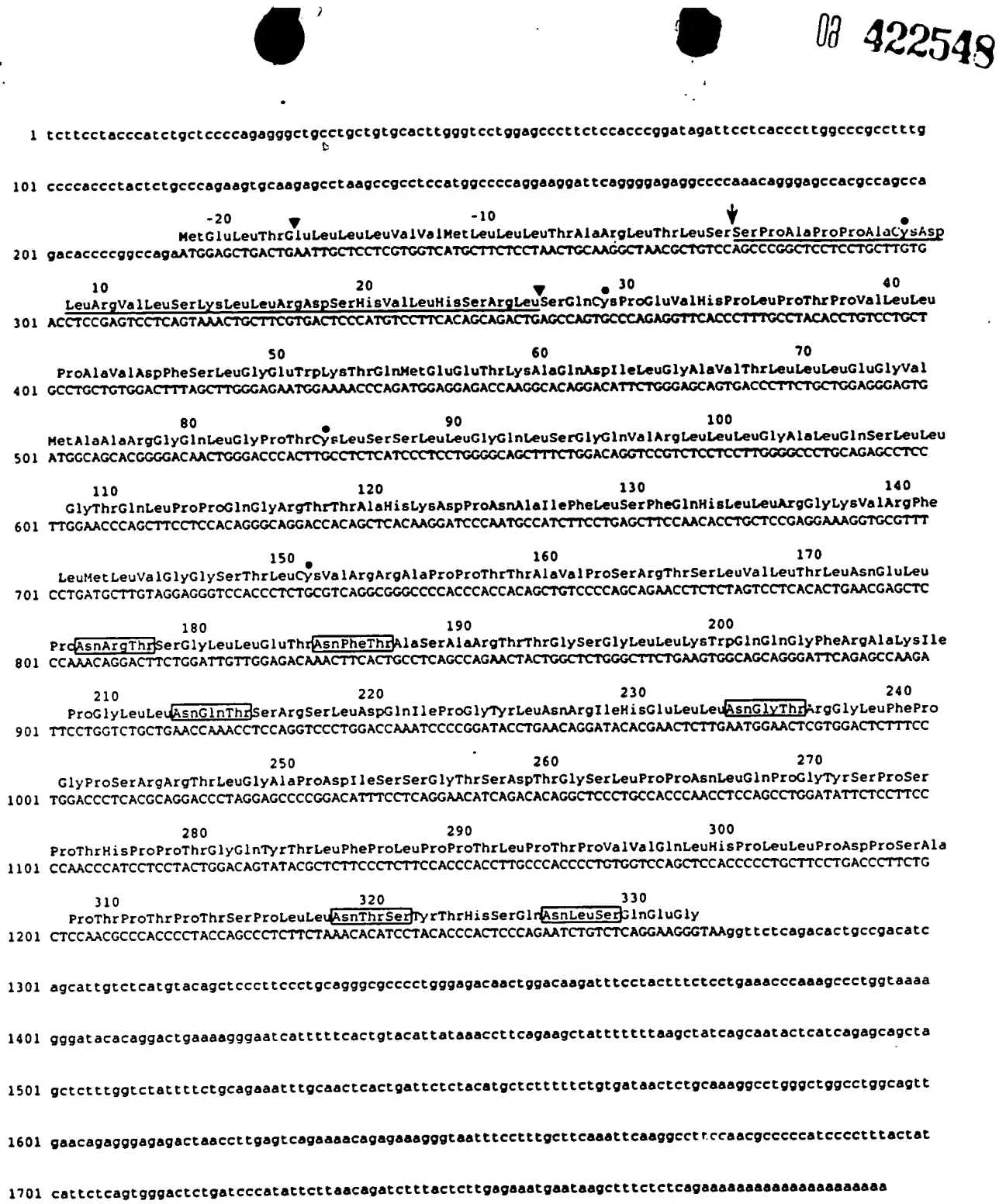

1 tcttcctacccatctgctccccagagggctgcctgctgtgcacttgggtcctggagcccttctccacccggatagattcctcacccttggcccgcctttg
101 ccccaccctactctgcccagaagtgcaagagcctaagccgcctccatggccccaggaaggattcaggggagaggccccaaacagggagccacgccagcca
-20 -10
MetGluLeuThrGluLeuLeuLeuValValMetLeuLeuLeuThrAlaArgLeuThrLeuSerSerProAlaProProAlaCysAsp
201 gacaccccggccagaATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTGTCCAGCCCGGCTCCTCCTGCTTGTG
10 20 30 40
LeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeu
301 ACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCT
50 60 70
ProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyVal
401 GCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTG
80 90 100
MetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu
501 ATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCC
110 120 130 140
GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPhe
601 TTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTT
150 160 170
LeuMetLeuValGlyGlySerThrLeuCysValArgArgAlaProProThrThrAlaValProSerArgThrSerLeuValLeuThrLeuAsnGluLeu
701 CCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGCGGGCCCCACCCACCACAGCTGTCCCCAGCAGAACCTCTCTAGTCCTCACACTGAACGAGCTC
180 190 200
ProAsnArgThrSerGlyLeuLeuGluThrAsnPheThrAlaSerAlaArgThrThrGlySerGlyLeuLeuLysTrpGlnGlnGlyPheArgAlaLysIle
801 CCAAACAGGACTTCTGGATTGTTGGAGACAAACTTCACTGCCTCAGCCAGAACTACTGGCTCTGGGCTTCTGAAGTGGCAGCAGGGATTCAGAGCCAAGA
210 220 230 240
ProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyTyrLeuAsnArgIleHisGluLeuLeuAsnGlyThrArgGlyLeuPhePro
901 TTCCTGGTCTGCTGAACCAAACCTCCAGGTCCCTGGACCAAATCCCCGGATACCTGAACAGGATACACGAACTCTTGAATGGAACTCGTGGACTCTTTCC
250 260 270
GlyProSerArgArgThrLeuGlyAlaProAspIleSerSerGlyThrSerAspThrGlySerLeuProProAsnLeuGlnProGlyTyrSerProSer
1001 TGGACCCTCACGCAGGACCCTAGGAGCCCCGGACATTTCCTCAGGAACATCAGACACAGGCTCCCTGCCACCCAACCTCCAGCCTGGATATTCTCCTTCC
280 290 300
ProThrHisProProThrGlyGlnTyrThrLeuProLeuProProThrLeuProThrProValValGlnLeuHisProLeuLeuProAspProSerAla
1101 CCAACCCATCCTCCTACTGGACAGTATACGCTCTTCCCTCTTCCACCCACCTTGCCCACCCCTGTGGTCCAGCTCCACCCCCTGCTTCCTGACCCTTCTG
310 320 330
ProThrProThrProThrSerProLeuLeuAsnThrSerTyrThrHisSerGlnAsnLeuSerGlnGluGly
1201 CTCCAACGCCCACCCCTACCAGCCCTCTTCTAAACACATCCTACACCCACTCCCAGAATCTGTCTCAGGAAGGGTAAggttctcagacactgccgacatc
1301 agcattgtctcatgtacagctcccttccctgcagggcgcccctgggagacaactggacaagatttcctactttctcctgaaacccaaagccctggtaaaa
1401 gggatacacaggactgaaaagggaatcatttttcactgtacattataaaccttcagaagctatttttttaagctatcagcaatactcatcagagcagcta
1501 gctctttggtctatttttctgcagaaatttgcaactcactgattctctacatgctctttttctgtgataactctgcaaaggcctgggctggcctggcagtt
1601 gaacagagggagagactaaccttgagtcagaaaacagagaaagggtaatttcctttgcttcaaattcaaggcctt ccaacgcccccatcccctttactat
1701 cattctcagtgggactctgatcccatattcttaacagatctttactcttgagaaatgaataagctttctctcagaaaaaaaaaaaaaaaaaaaaa

Figure 8

Figure 9

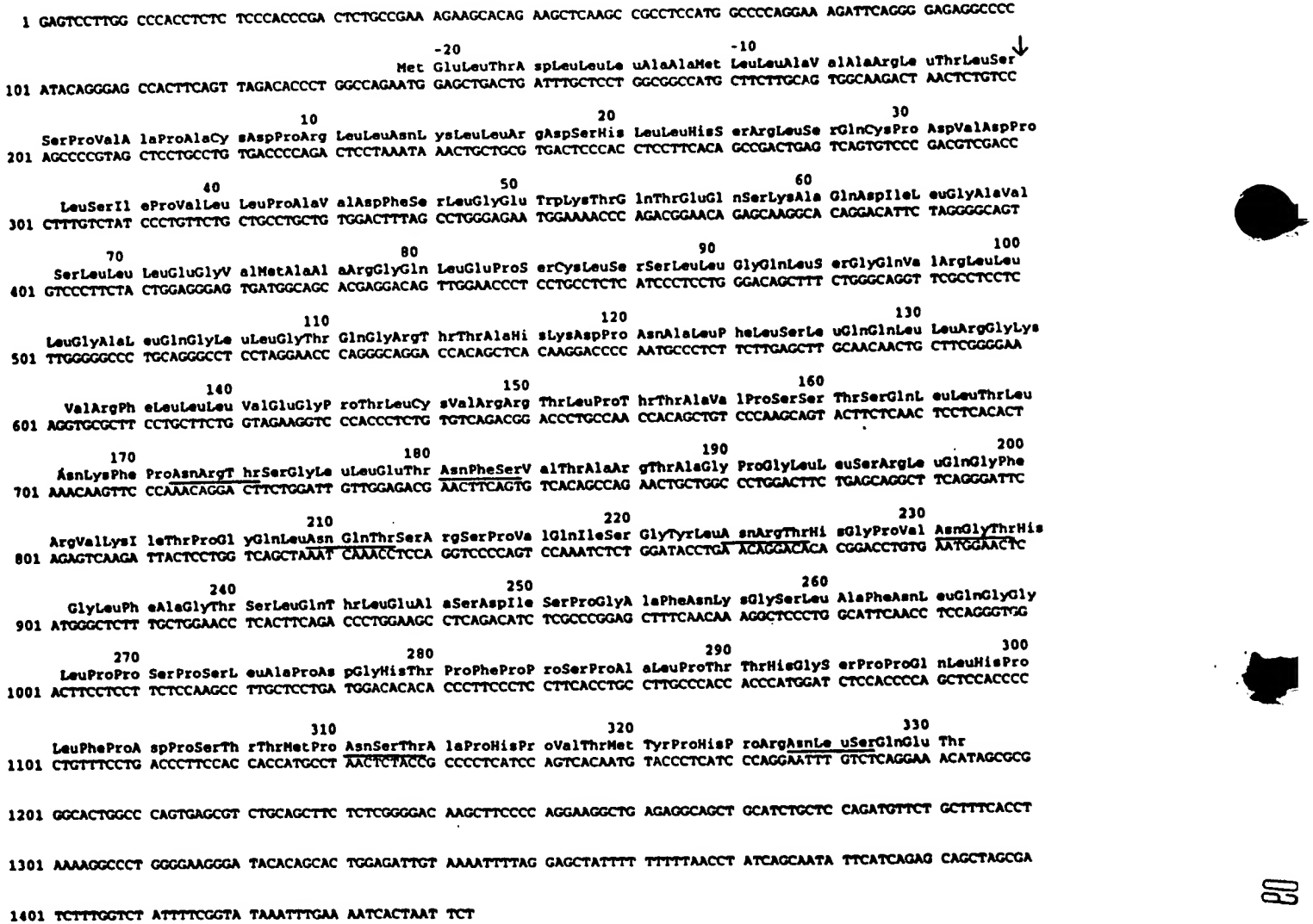


Figure 10

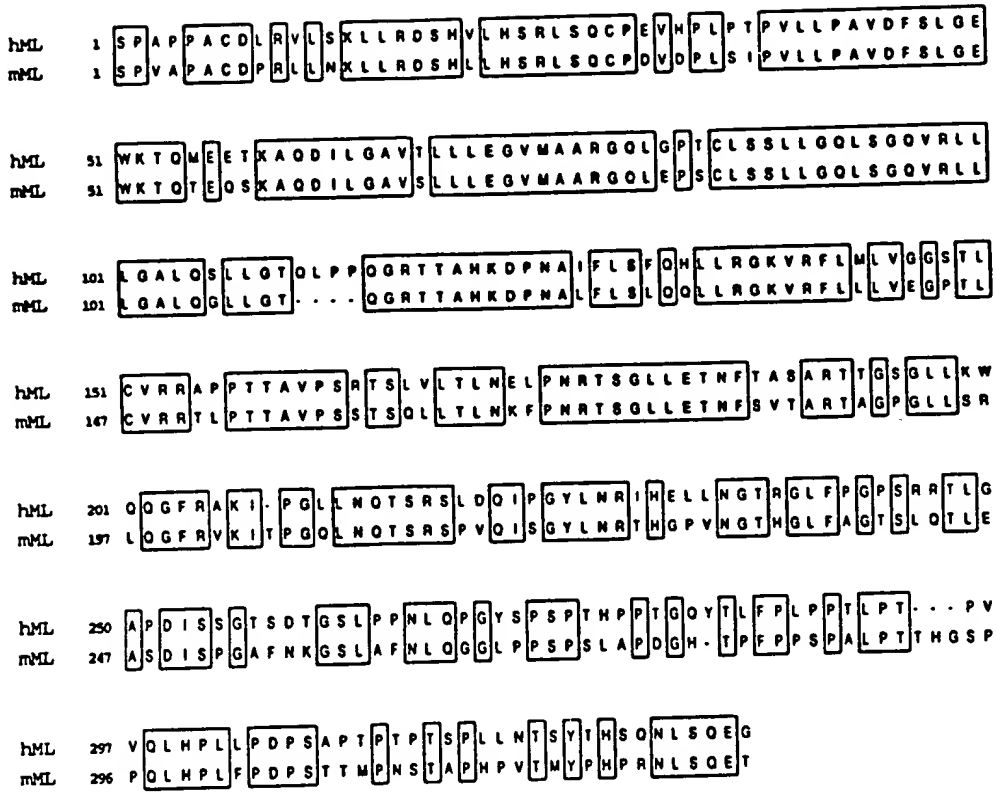
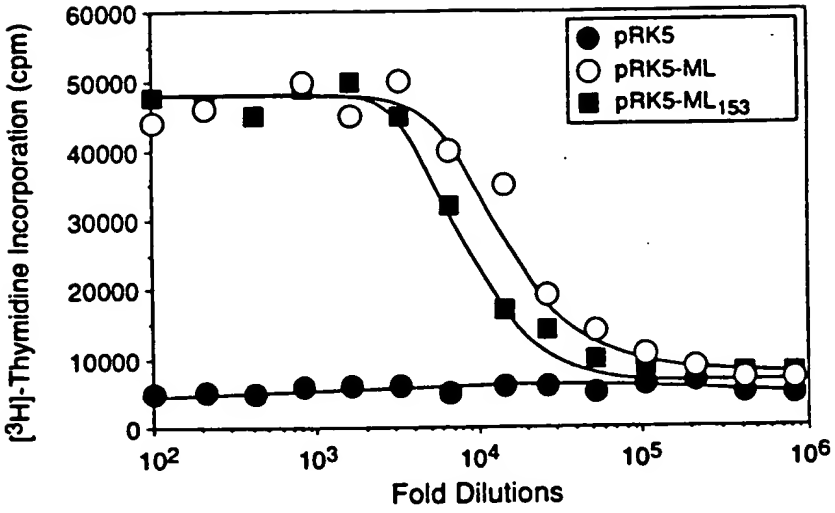
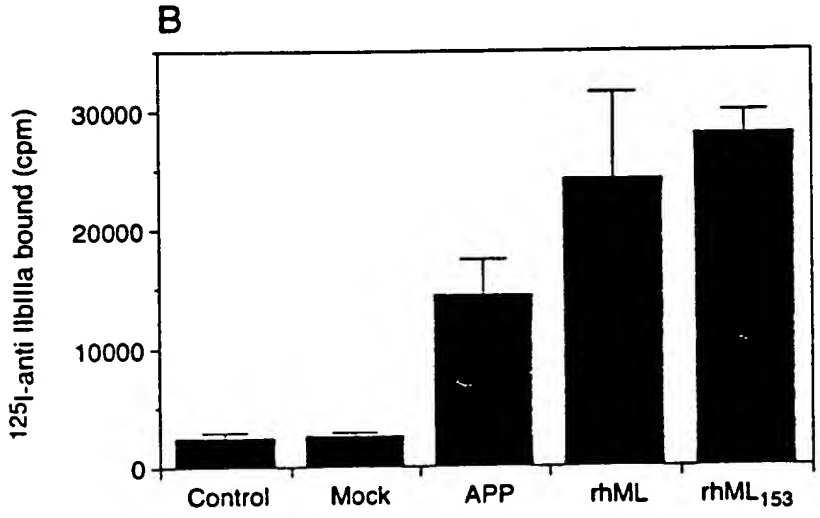


Figure 11


60000
50000
40000
30000
20000
10000
0
[3H]-Thymidine Incorporation (cpm)
pRK5
pRK5-ML
pRK5-ML153
10^2
10^3
10^4
10^5
10^6
Fold Dilutions


B
30000
20000
10000
0
125I-anti IIbIIIa bound (cpm)
Control
Mock
APP
rhML
rhML153

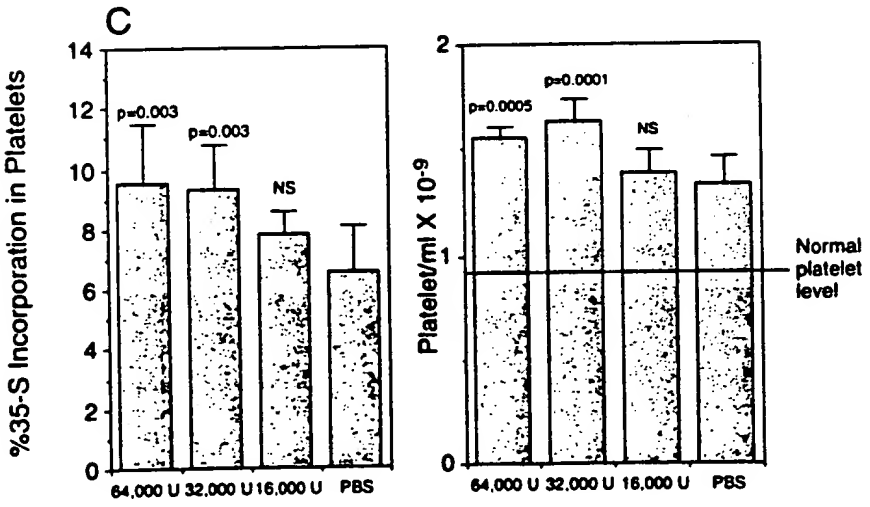

C
14
12
10
8
6
4
2
0
%35-S Incorporation in Platelets
p=0.003
p=0.003
NS
64,000 U
32,000 U
16,000 U
PBS
2
1
0
Platelet/ml X 10-9
p=0.0005
p=0.0001
NS
Normal platelet level
64,000 U
32,000 U
16,000 U
PBS

Figure 12